

Metagenomic Mining of Glycoside Hydrolases from the Hindgut Bacterial Symbionts of a Termite, Trinervitermise trinervoides and the Characterisation of a Multimodular -1, 4-Xylanase (GH11)



Journal:	Biotechnology and Applied Biochemistry
Manuscript ID	Draft
Wiley - Manuscript type:	Original Article
Date Submitted by the Author:	n/a
Complete List of Authors:	Rashamuse, Konanani; CSIR, Biosciences Sanyika, Tendai; Chinhoyi University of Technology, Biotechnology Mathiba, Kgama; CSIR, Biosciences Ngcobo, Thobile; CSIR, Biosciences Mtimka, Sibongile; CSIR-Pretoria, Biosciences Brady, Dean; University of Witswaterstrand, School of Chemistry
Keywords:	Metagenomics, Termite Hindgut, Gene discovery
Mandatory Keywords:	Biocatalysis, Purification, Recombinant Protein, Enzyme
Abstract:	<p>In recent years, there have been particular emphases worldwide on the development and optimization of bioprocesses for the utilization of biomass. An essential component of the biomass processing conduit has been the need for robust biocatalysts as high-performance tools for both the depolymerisation of lignocellulosic biomass, and synthesis of new high-value biobased chemical entities. Through functional screening of the metagenome of the Hindgut Bacterial Symbionts of a Termite, Trinervitermise trinervoides we discovered ORFs for 25 cellulases and hemicellulases. These were classified into 14 different GH families: eight GH family 5; four GHF9, two GH13 and one each in GH2, GH10, GH11, GH26, GH29, GH43, GH44, GH45, GH67 and GH94 families. The GH11 (Xyl1) was of particular interest as it was discovered to be a multimodular -1, 4-Xylanase, consisting of a catalytic domain and two carbohydrate binding modules. This endo-xylanase was optimal at pH 6 and 50 °C, and generated xylobiose and xylotriose from various xylan sources, including beechwood, birchwood and wheat arabinoxylan. The catalytic ability of GH11 against natural substrate (such as wheat arabinoxylan) renders GH11 as a potential useful biocatalyst in the effective dismantling of complex plant biomass architecture.</p>

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